OIPE

RAW SEQUENCE LISTING   DATE: 01/08/2002
PATENT APPLICATION: US/09/893,512   TIME: 16:00:04

Input Set : A:\76750001.app
Output Set: N:\CRF3\01082002\I893512.raw   ENTERED

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 3 <110> APPLICANT: OWMAN, CHRISTER
 5 <120> TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
 6       RECEPTOR
 8 <130> FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
10 <140> CURRENT APPLICATION NUMBER: 09/893,512
11 <141> CURRENT FILING DATE: 2001-06-29
13 <150> PRIOR APPLICATION NUMBER: 60/061,789
14 <151> PRIOR FILING DATE: 1997-10-14
16 <150> PRIOR APPLICATION NUMBER: 60/081,958
17 <151> PRIOR FILING DATE: 1998-04-15
19 <150> PRIOR APPLICATION NUMBER: 09/170,069
20 <151> PRIOR FILING DATE: 1998-10-13
22 <160> NUMBER OF SEQ ID NOS: 17
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1672
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 1
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34 ggttgccctg gaaaacagac tatccccct cctagtgaag ggagtgggta ggggtttcag 180
35 ccccaccctc aggaagatgc gtcttccctg tcctctgctc tgtggtactt cctctctggc 240
36 tgatttagca aacagcacct agacctgggc caggcctttg gcagtgggac agatccaggg 300
37 ataggctaca ccaccctgcc ctgaccctgg gattggcatc agcttccaac cagttcctgc 360
38 caaagcttgt aaggtcctcc cgacggccat gaacactaca tcttctgcag cacccccctc 420
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40 ggggcttccc ggcaacagct ttgtggtgtg gagtatcctg aaaaggatgc agaagcgctc 540
41 tgtcactgcc ctgatggtgc tgaacctggc cctggccgac ctggccgtat tgctcactgc 600
42 tccctttttc cttcacttcc tggcccaagg cacctggagt tttggactgg ctggttgccg 660
43 cctgtgtcac tatgtctgcg gagtcagcat gtacgccagc gtcctgctta tcacggccat 720
44 gagtctagac cgctcactgg cggtggcccg ccccttgtg tcccagaagc tacgcaccaa 780
45 ggcgatggcc cggcgggtgc tggcaggcat ctgggtgttg tcctttctgc tggccacacc 840
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47 gtaccccagc gaagggcacc gggccttcca tctaatcttc gaggctgtca cgggcttcct 960
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57 gttcagtacc tggaggagga gcaggggcgt ggagggcgtg gagggcgtgg agcgtgggga 1560
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63 <211> LENGTH: 352
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
67 <400> SEQUENCE: 2
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71 Ile Ser Leu Leu Ala Ile Ile Leu Leu Ser Val Ala Leu Ala Val Gly
72             20                  25                  30
74 Leu Pro Gly Asn Ser Phe Val Val Trp Ser Ile Leu Lys Arg Met Gln
75         35                  40                  45
77 Lys Arg Ser Val Thr Ala Leu Met Val Leu Asn Leu Ala Leu Ala Asp
78         50                  55                  60
80 Leu Ala Val Leu Leu Thr Ala Pro Phe Phe Leu His Phe Leu Ala Gln
81  65                  70                  75                  80
83 Gly Thr Trp Ser Phe Gly Leu Ala Gly Cys Arg Leu Cys His Tyr Val
84             85                  90                  95
86 Cys Gly Val Ser Met Tyr Ala Ser Val Leu Leu Ile Thr Ala Met Ser
87             100                 105                 110
89 Leu Asp Arg Ser Leu Ala Val Ala Arg Pro Phe Val Ser Gln Lys Leu
90         115                 120                 125
92 Arg Thr Lys Ala Met Ala Arg Arg Val Leu Ala Gly Ile Trp Val Leu
93         130                 135                 140
95 Ser Phe Leu Leu Ala Thr Pro Val Leu Ala Tyr Arg Thr Val Val Pro
96 145                 150                 155                 160
98 Trp Lys Thr Asn Met Ser Leu Cys Phe Pro Arg Tyr Pro Ser Glu Gly
99                 165                 170                 175
101 His Arg Ala Phe His Leu Ile Phe Glu Ala Val Thr Gly Phe Leu Leu
102             180                 185                 190
104 Pro Phe Leu Ala Val Val Ala Ser Tyr Ser Asp Ile Gly Arg Arg Leu
105         195                 200                 205
107 Gln Ala Arg Arg Phe Arg Arg Ser Arg Arg Thr Gly Arg Leu Val Val
108     210                 215                 220
110 Leu Ile Ile Leu Thr Phe Ala Ala Phe Trp Leu Pro Tyr His Val Val
111 225                 230                 235                 240
113 Asn Leu Ala Glu Ala Arg Arg Ala Leu Ala Gly Gln Ala Ala Gly Leu
114                 245                 250                 255
116 Gly Leu Val Gly Lys Arg Leu Ser Leu Ala Arg Asn Val Leu Ile Ala
117             260                 265                 270
119 Leu Ala Phe Leu Ser Ser Ser Val Asn Pro Val Leu Tyr Ala Cys Ala
120         275                 280                 285
122 Gly Gly Gly Leu Leu Arg Ser Ala Gly Val Gly Phe Val Ala Lys Leu
123     290                 295                 300
125 Leu Glu Gly Thr Gly Ser Glu Ala Ser Ser Thr Arg Arg Gly Gly Ser
126 305                 310                 315                 320
128 Leu Gly Gln Thr Ala Arg Ser Gly Pro Ala Ala Leu Glu Pro Gly Pro
129                 325                 330                 335
131 Ser Glu Ser Leu Thr Ala Ser Ser Pro Leu Lys Leu Asn Glu Leu Asn
132             340                 345                 350
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Input Set : A:\76750001.app
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139 <211> LENGTH: 27
140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 3
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147 <210> SEQ ID NO: 4
148 <211> LENGTH: 29
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 4
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156 <210> SEQ ID NO: 5
157 <211> LENGTH: 48
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 5
162 acacaggagg caaccagcca gtccaaaact ccaggtgcct tgggccag    48
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 48
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens
170 <400> SEQUENCE: 6
171 gatcggtgcc agcacccgcc gggccatcgc cttggtgcgt agcttctg    48
174 <210> SEQ ID NO: 7
175 <211> LENGTH: 8
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <221> NAME/KEY: VARIANT
181 <222> LOCATION: (3)
182 <223> OTHER INFORMATION: Xaa at position 3 is any amino acid
184 <400> SEQUENCE: 7
185 Gly Asn Xaa Leu Val Val Leu Val
186    1            5
189 <210> SEQ ID NO: 8
190 <211> LENGTH: 18
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <220> FEATURE:
195 <221> NAME/KEY: VARIANT
196 <222> LOCATION: (6)
197 <223> OTHER INFORMATION: Xaa at position 6 is any amino acid
199 <220> FEATURE:
200 <221> NAME/KEY: VARIANT
201 <222> LOCATION: (7)
202 <223> OTHER INFORMATION: Xaa at position 7 is any amino acid
204 <220> FEATURE:
205 <221> NAME/KEY: VARIANT
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206 <222> LOCATION: (12)
207 <223> OTHER INFORMATION: Xaa at position 12 is any amino acid
209 <220> FEATURE:
210 <221> NAME/KEY: VARIANT
211 <222> LOCATION: (13)
212 <223> OTHER INFORMATION: Xaa at position 13 is any amino acid
214 <220> FEATURE:
215 <221> NAME/KEY: VARIANT
216 <222> LOCATION: (17)
217 <223> OTHER INFORMATION: Xaa at position 17 is any amino acid
219 <400> SEQUENCE: 8
220 Leu Leu Asn Leu Ala Xaa Xaa Asp Leu Leu Phe Xaa Xaa Thr Leu Pro
221   1               5                  10                  15
223 Xaa Trp
227 <210> SEQ ID NO: 9
228 <211> LENGTH: 350
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 9
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234   1               5                  10                  15
236 Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys Met Leu
237              20              25              30
239 Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu
240              35              40              45
242 Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
243         50              55              60
245 Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr Leu Leu Asn
246   65              70              75                  80
248 Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro Ile Trp Ala
249              85              90                  95
251 Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu Cys Lys Val
252             100             105             110
254 Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu
255             115             120             125
257 Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala Thr Arg
258      130             135             140
260 Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys
261 145             150             155             160
263 Trp Gly Leu Ser Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln
264             165             170             175
266 Ala Tyr His Pro Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly
267             180             185             190
269 Asn Asp Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr
270             195             200             205
272 Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe
273      210             215             220
275 Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala
276 225             230             235             240
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Input Set : A:\76750001.app
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278 Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu
279                 245             250             255
281 Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val
282             260             265             270
284 Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg Ala Leu Asp
285         275             280             285
287 Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu Asn Pro Ile Ile
288     290             295             300
290 Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly Phe Leu Lys Ile Leu
291 305             310             315                     320
293 Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val
294             325             330             335
296 Thr Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu
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301 <211> LENGTH: 355
302 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
305 <400> SEQUENCE: 10
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310             20              25              30
312 Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile
313         35              40              45
315 Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
316     50              55              60
318 Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val
319 65              70              75                      80
321 Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu
322             85              90              95
324 Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe
325             100             105             110
327 Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly
328         115             120             125
330 Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val
331     130             135             140
333 His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile
334 145             150             155             160
336 Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu
337             165             170             175
339 Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr
340         180             185             190
342 Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile
343         195             200             205
345 Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe
346     210             215             220
348 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln
349 225             230             235             240
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VERIFICATION SUMMARY   DATE: 01/08/2002
PATENT APPLICATION: US/09/893,512   TIME: 16:00:05

          Input Set : A:\76750001.app
          Output Set: N:\CRF3\01082002\I893512.raw

L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8